



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/080,959
Source: O/P
Date Processed by STIC: 3/11/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/080,959

DATE: 03/11/2002

TIME: 10:19:07

Input Set : A:\EP.txt

Output Set: N:\CRF3\03112002\J080959.raw

Does not contain
errors

2 <110> APPLICANT: Cruz-Perez, Patricia
3 Buttner, Mark P.
W--> 4 <120> TITLE OF INVENTION: Method for Detection of Stachybotrys chartarum in Pure Culture and Field
W--> 5 Samples Using Quantitative Polymerase Chain Reaction
W--> 6 <130> FILE REFERENCE: 0001-00001
W--> 7 <140> CURRENT APPLICATION NUMBER:
C--> 8 <141> CURRENT FILING DATE: 2002-02-22
9 <150> PRIOR APPLICATION NUMBER: US 60/280,712
10 <151> PRIOR FILING DATE: 2001-03-29
W--> 11 <160> NUMBER OF SEQ ID: 5

ERRORED SEQUENCES

W--> 12 <210> SEQ ID NO: 1
13 <211> LENGTH: 17
14 <212> TYPE: DNA
15 <213> ORGANISM: Stachybotrys chartarum

W--> 16 <220> FEATURE:
W--> 17 <221> NAME/KEY:
18 <222> LOCATION:
19 <223> OTHER INFORMATION:

E--> 20 <400> 1
E--> 20 gttgcttcggcggaac
21 <210> SEQ ID NO: 2
22 <211> LENGTH: 20
23 <212> TYPE: DNA
24 <213> ORGANISM: Stachybotrys chartarum

W--> 25 <220> FEATURE:
W--> 26 <221> NAME/KEY:
27 <222> LOCATION:
28 <223> OTHER INFORMATION:

E--> 29 <400> SEQUENCE: 0
E--> 29 ttgcggttgccactcagag
30 <210> SEQ ID NO: 3

W--> 35 <220> FEATURE:
W--> 36 <221> NAME/KEY:
37 <222> LOCATION:
38 <223> OTHER INFORMATION:
E--> 38 <400> SEQUENCE: 0

(global error)

The <400> line is separate, and must
only indicate the
sequence ID NO

Per 1000 sequence rule,
all non-coding nucleotide
sequences must be grouped
with 10's with the same

must be same as the
sequence

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/080,959

DATE: 03/11/2002

TIME: 10:19:07

Input Set : A:\EP.txt

Output Set: N:\CRF3\03112002\J080959.raw

E--> 38 acctatcggttgcttcggcg *same*
39 <210> SEQ ID NO: 4
40 <211> LENGTH: 23
41 <212> TYPE: DNA
42 <213> ORGANISM: Stachybotrys chartarum
W--> 43 <220> FEATURE:
W--> 44 <221> NAME/KEY:
45 <222> LOCATION: *same*
46 <223> OTHER INFORMATION:
E--> 47 <400> SEQUENCE: 0
E--> 47 gcgtttgccactcagagaataact
48 <210> SEQ ID NO: 5
49 <211> LENGTH: 18
50 <212> TYPE: DNA
51 <213> ORGANISM: Stachybotrys chartarum
W--> 52 <220> FEATURE:
W--> 53 <221> NAME/KEY:
54 <222> LOCATION:
55 <223> OTHER INFORMATION: *same*
E--> 56 <400> SEQUENCE: 0
E--> 56 ctgcgcccgatccaggc

Please see sample Sequence Listings
(attached) for valid format.

Also, please consult Sequence Rules

<110> Smith, John; Smithgene Inc.
 <120> Example of a Sequence Listing
 <130> 01-00001
 <140> PCT/EP98/00001
 <141> 1998-12-31
 <150> US 08/999,999
 <151> 1997-10-15
 <160> 4
 <170> PatentIn version 2.0
 <210> 1
 <211> 389
 <212> DNA
 <213> Paramecium sp.
 <220>
 <221> CDS
 <222> (279)...(389)
 <300>
 <301> Doe, Richard
 <302> Isolation and Characterization of a Gene Encoding a
 Protease from Paramecium sp.
 <303> Journal of Genes
 <304> 1
 <305> 4
 <306> 1-7
 <307> 1988-06-31
 <308> 123456
 <309> 1988-06-31
 <400> 1
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 agggagagtg tcttgacctt cctctgcctt tgcagcttca caggcaggca ggcaggcagc 120
 tcatgtggca attgctggca gtgccacagg ctttctagcc aggccttaggg tgggttcgc 180
 cgcggcgagg cggccctctt cgcgctcttc tcgcgctctt ctctcgtctt cctctcgtct 240

once consult

Appendix 3, page 2

ggacctgatt aggtgagcag gaggaggggg cagtttagc atg gtt tca atg ttc agc 296
Met Val Ser Met Phe Ser

ttg	tct	ttc	aaa	tgg	cct	gga	ttt	tgt	ttg	ttt	gtt	tgt	ttg	ttc	caa	344
Leu	Ser	Phe	Lys	Trp	Pro	Gly	Phe	Cys	Leu	Phe	Val	Cys	Leu	Phe	Gln	
			10					15					20			

tgt	ccc	aaa	gtc	ctc	ccc	tgt	cac	tca	tca	ctg	cag	ccg	aat	ctt			189
Cys	Pro	Lys	Val	Leu	Pro	Cys	His	Ser	Ser	Leu	Gln	Pro	Asn	Leu			
		25					30					35					

<210>	2
<211>	37
<212>	PRT
<213>	Paramecium sp.

Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu
1 5 10 15

Phe Val Cys Leu Phe Gln Cys Pro Lys Val Leu Pro Cys His Ser Ser
20 25 30

Leu Gln Pro Asn Leu
 35

```

<210>      )
<211>      11
<212>      PART
<213>      Artificial Sequence

```

<220>	
<221>	Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ

<400>										
Met	Val	Asn	Leu	Glu	Pro	Met	His	Thr	Glu	Ile
1				5					10	

<210>	4
<400>	4
000	

[Annex VIII follows]

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M, when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO: #:	Response shall be an integer representing the SEQ ID NO shown	M

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<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location	M, under the fol-
		bases/amino acids	acid or modified

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		in feature	was used in sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MM-yyyy	0
<310>	Patent Document	Document number;	0

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	0
<313>	Relevant Residues	FROM (position) TO (position)	0
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	M

5. Section 1.024 is revised to read as follows:

1.024 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.021(c) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format

operating system: DOS, Macintosh, UNIX or Macintosh.

VERIFICATION SUMMARY

DATE: 03/11/2002

PATENT APPLICATION: US/10/080,959

TIME: 10:19:08

Input Set : A:\EP.txt

Output Set: N:\CRF3\03112002\J080959.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:283 W: Missing Blank Line separator, <140> field identifier
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:11 M:283 W: Missing Blank Line separator, <160> field identifier
L:12 M:283 W: Missing Blank Line separator, <210> field identifier
L:16 M:283 W: Missing Blank Line separator, <220> field identifier
L:17 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:20 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:0
L:20 M:283 W: Missing Blank Line separator, <400> field identifier
L:20 M:252 E: No. of Seq. differs, <211>LENGTH:Input:17 Found:0 SEQ:1
L:25 M:283 W: Missing Blank Line separator, <220> field identifier
L:26 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:29 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:0
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:29 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:0 SEQ:2
L:34 M:283 W: Missing Blank Line separator, <220> field identifier
L:35 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:38 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:0
L:38 M:283 W: Missing Blank Line separator, <400> field identifier
L:38 M:252 E: No. of Seq. differs, <211>LENGTH:Input:19 Found:0 SEQ:3
L:43 M:283 W: Missing Blank Line separator, <220> field identifier
L:44 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:47 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:0
L:47 M:283 W: Missing Blank Line separator, <400> field identifier
L:47 M:252 E: No. of Seq. differs, <211>LENGTH:Input:23 Found:0 SEQ:4
L:52 M:283 W: Missing Blank Line separator, <220> field identifier
L:53 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:56 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:5 differs:0
L:56 M:283 W: Missing Blank Line separator, <400> field identifier
L:56 M:252 E: No. of Seq. differs, <211>LENGTH:Input:18 Found:0 SEQ:5